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<212> DNA
<213> Homo sapiens

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taggcataga gccaggactg tttgggtaaa ctggtcactt tatcttaaac taaatatatc 540

caaaactgaa catgtactta gttactaagt ctttgacttt atctcattca taccactcag 600

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gctgttaatt attggcaaat gtcccatttt caacctaagg aaataccata aagtaacaga 720

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<211> 472
<212> DNA
<213> Homo sapiens

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<210> 8
<211> 858
<212> DNA
<213> Homo sapiens

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<213> Homo sapiens

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ctgattggag gaatggataa tagtcatcat gtttaaacat ctaccattcc agttaagaaa 180

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gaacctattt gtatactaga tgacacaatg tcaatgtctg tgtacaactg ccaactggga 360

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<213> Homo sapiens

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<222> (2)..(304)

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  Met Thr Gly Ser Thr Ile Ala Pro Thr Thr Asp Tyr Arg Asn Thr Thr
    1               5                  10                  15

gct acc gga cta aca tct gcc cta aat tta ccc caa gtt cat gcc ttt   97
Ala Thr Gly Leu Thr Ser Ala Leu Asn Leu Pro Gln Val His Ala Phe
            20                  25                  30

gtc aat gac tgg gcg agc ttg gac atg tgg tgg ttt tcc ata gcg ctt   145
Val Asn Asp Trp Ala Ser Leu Asp Met Trp Trp Phe Ser Ile Ala Leu
        35                  40                  45

atg ttt gtt tgc ctt att att atg tgg ctt att tgt tgc cta aag cgc   193
Met Phe Val Cys Leu Ile Ile Met Trp Leu Ile Cys Cys Leu Lys Arg
    50                  55                  60

aga cgc gcc aga ccc ccc atc tat agg cct atc att gtg ctc aac cca   241
Arg Arg Ala Arg Pro Pro Ile Tyr Arg Pro Ile Ile Val Leu Asn Pro
65                  70                  75                  80

cac aat gaa aaa att cat aga ttg gac ggt ctg aaa cca tgt tct ctt   289
His Asn Glu Lys Ile His Arg Leu Asp Gly Leu Lys Pro Cys Ser Leu
                85                  90                  95

ctt tta cag tat gat taa                                          307
Leu Leu Gln Tyr Asp
            100


<210> 11
<211> 101
<212> PRT
<213> Homo sapiens

<400> 11
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  1               5                  10                  15

Ala Thr Gly Leu Thr Ser Ala Leu Asn Leu Pro Gln Val His Ala Phe
            20                  25                  30

Val Asn Asp Trp Ala Ser Leu Asp Met Trp Trp Phe Ser Ile Ala Leu
        35                  40                  45

Met Phe Val Cys Leu Ile Ile Met Trp Leu Ile Cys Cys Leu Lys Arg
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50 55 60

Arg Arg Ala Arg Pro Pro Ile Tyr Arg Pro Ile Ile Val Leu Asn Pro
65 70 75 80

His Asn Glu Lys Ile His Arg Leu Asp Gly Leu Lys Pro Cys Ser Leu
85 90 95

Leu Leu Gln Tyr Asp
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<213> Unknown

<220>
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<211> 23
<212> DNA
<213> Unknown

<220>
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<400> 13
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<210> 14
<211> 19
<212> DNA
<213> Unknown

<220>
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<400> 14
tcgtcttcaa gaattctca 19

<210> 15
<211> 20
<212> DNA
<213> Unknown

<220>
<223> Description of Unknown Organism: unknown

<400> 15
tttcagtcac cggtgtcgga 20

<210> 16

<211> 20
<212> DNA
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<220>
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<400> 16
gcattctcta gacacaggtg 20

<210> 17
<211> 22
<212> DNA
<213> Unknown

<220>
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<400> 17
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<210> 18
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<212> DNA
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<210> 19
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<400> 19
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<211> 26
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<213> Unknown

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<212> DNA
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<210> 22
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<220>
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aaactgaata agactcttcg aaatctgaat aattttgtgt tactcatagc gcgtaatatt 120

tgtctagggc cgcggggact ttgaccgttt acgtgg 156

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<211> 156
<212> DNA
<213> Unknown

<220>
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cttactcggt tacgcccaaa tttactacaa catccc 156

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<210> 31
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<400> 37
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<400> 41
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<213> Unknown

<220>
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<400> 43
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aaaatttgct gttcttcatg gtttctcttt tcactgctat ctatttttct caaccactca 180

catggctaca ataactgtct gcaagcttat gattcccaaa tatctatctc tagcctcaat 240

cttgttccag aagataaaaa gtagtattca aatgcacatc aacgtctcca cttggagggc 300

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tcccacctat ggggagatga gagtgaaaag ggagcctgat taataattac actaagtcaa 480

taggcataga gccaggactg tttgggtaaa ctggtcactt tatcttaaac taaatatatc 540

caaaactgaa catgtactta gttactaagt ctttgacttt atctcattca taccactcag 600

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<220>
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acaagaggtt ccatgagaaa ataatctgaa aggtttaata agttgtcaaa ggtgagaggg 660

ctcttctcta gctagagact aatcagaaat acattcaggg ataattattt gaatagacct 720

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attttcaact aaccaaccac ccaatccaac aaacaaaaaa tgaaaagaat ctcagaaaca 840

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cagaggtcag cactggggaa gacaggttgt cctcccaggg gatgggggtc catccacctt 240

gccgaaaaga tttgtctgag gaactgaaaa tagaagggaa aaaagaggag ggacaaaaga 300

ggcagaaatg agaggggagg ggacagagga cacctgaata aagaccacac ccatgaccca 360

cgtgatgctg agaagtactc ctgccctagg aagagactca gggcagaggg aggaaggaca 420

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<210> 56
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<210> 58
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<220>
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catgtggtgg ttttccatag cgcttatgtt tgtttgcctt attattatgt ggcttatttg 180

ttgcctaaag cgcagacgcg ccagaccccc catctatagg cctatcattg tgctcaaccc 240

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